

1 ATGAAGTTGCCTGTTAGGCTGTTGGTGCTTCTGTTGTTCTGGATTCTGTTTCCGGAGGT 60  
-----  
TACTTCAACGGACAATCCGACAACCACGAAGACAACAAGACCTAAGGACAAAGGCCTCCA  
[M K L P V R L L V L L L F W I P V S G G]

Signal Peptide

61 GATGTTGTGGTGA CTCAA CTCTCCCTGCCTGTCAGCTTTGGAGATCAAGTTTCT 120  
-----  
CTACAACACCACTGAGTTTGAGGTGAGAGGGACGGACAGTCGAAACCTCTAGTTCAAAGA  
[D V V V T Q T P L S L P V S F G D Q V S]

Framework 1

121 ATCTCTTG CAGGTCTAGTCAGAGTCTTGCAAAGAGTTATGGGAACACCTATTTGTCTTGG 180  
-----  
TAGAGAACGTCCAGATCAGTCTCAGAACGTTTCTCAATACCCTTGTGGATAAACAGAACC  
I S C][R S S Q S L A K S Y G N T Y L S][W

CDR 1

181 TACCTGCACAAGCCTGGCCAGTCTCCACAGCTCCTCATCTATGGGATTTCCAACAGATTT 240  
-----  
ATGGACGTGTTCCGACCGGTGTCAGAGGTGTCGAGGAGTAGATAACCCTAAAGGTTGTCTAAA  
Y L H K P G Q S P Q L L I Y][G I S N R F

Framework 2 CDR 2

241 TCTGGGGTGCCAGACAGGTTTCAGTGGCAGTGGTTTCAGGGACAGATTTCACTCAAGATC 300  
-----  
AGACCCCAACGGTCTGTCCAAGTCACCGTCACCAAGTCCCTGTCTAAAGTGTGAGTTCTAG  
S][G V P D R F S G S G S G T D F T L K I

Framework 3

301 AGCACAATAAAGCCTGAGGACTTGGGAATGTATTACTGCTTACAAGGTACACATCAGCCG 360  
-----  
TCGTGTTATTTCCGACTCCTGAACCCTTACATAATGACGAATGTTCCATGTGTAGTCGGC  
S T I K P E D L G M Y Y C][L Q G T H Q P

CDR 3

361 TACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAA  
-----  
ATGTGCAAGCCTCCCCCTGGTTTCGACCTTTATTTT  
Y T][F G G G T K L E I K]

Framework 4

FIG. 1

1 ATGGGATGGAGCTGTATCATCCTCTTCTTGGTATCAACAGCTACAAGTGTCCACTCCCAG 60  
-----  
TACCCCTACCTCGACATAGTAGGAGAAGAACCATAGTTGTTCGATGTTTCACAGGTGAGGGTC  
M G W S C I I L F L V S T A T S V H S][Q

Signal Peptide

61 GTCCAACTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGACTTCACTGAAGCTGTCC 120  
-----  
CAGGTTGACGTCGTCGGACCCCGACTCGAACACTTCGGACCCTGAAGTCACTTCGACAGG  
V Q L Q Q P G A E L V K P G T S V K L S

Framework 1

121 TGCAAGGGTTATGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCT 180  
-----  
ACGTTCCCAATACCGATGTGGAAGTGGTCGATGACCTACGTGACCCACTTCGTCTCCGGA  
C K G Y G Y T F T][S Y W M H][W V K Q R P

CDR 1

181 GGACAAGGCCTTGAGTGGATCGGAGAGATTGATCCTTCTGAGAGTAATACTAACTACAAT 240  
-----  
CCTGTTCCGGAACCTCACCTAGCCTCTCTAACTAGGAAGACTCTCATTATGATTGATGTTA  
G Q G L E W I G][E I D P S E S N T N Y N

Framework 2 CDR 2

241 CAAAAATTCAAGGGCAAGGCCACATTGACTGTAGACATTTCTCCAGCACAGCCTACATG 300  
-----  
GTTTTTAAGTTCCCGTTCCGGTGTAAGTGAACATCTGTAAAGGAGGTTCGTGTCGGATGTAC  
Q K F K G][K A T L T V D I S S S T A Y M

Framework 3

301 CAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTACTATTGTGCAAGAGGGGGTTAC 360  
-----  
GTCGAGTCGTCGGACTGTAGACTCCTGAGACGCCAGATGATAACACGTTCTCCCCCAATG  
Q L S S L T S E D S A V Y Y C A R][G G Y

361 GACGGATGGGACTATGCTATTGACTACTGGGGTCAAGGCACCTCAGTCACCGTCTCCTCA 420  
-----  
CTGCCTACCCTGATACGATAACTGATGACCCAGTTCGGTGGAGTCAGTGGCAGAGGAGT  
D G W D Y A I D Y][W G Q G T S V T V S S]

CDR 3 Framework 4

FIG. 2

```

      10      20      30      40
      *      *      *      *
ATG AAA TGC ACC TGG GTC ATT CTC TTC TTG GTA TCA ACA GCT ACA AGT
M   K   C   T   W   V   I   L   F   L   V   S   T   A   T   S>
      signalpeptide cleavage site
50      60      70      80      90
*      *      *      *      *
GTC CAC TCC CAG GTC CAA CTA GTG CAG TCT GGG GCT GAG GTT AAG AAG
V   H   S   Q   V   Q   L   V   Q   S   G   A   E   V   K   K

      100      110      120      130      140
      *      *      *      *      *
CCT GGG GCT TCA GTG AAG GTG TCC TGC AAG GGT TCT GGC TAC ACC TTC
P   G   A   S   V   K   V   S   C   K   G   S   G   Y   T   F>
                        Xba I

      150      160      170      180      190
      *      *      *      *      *
ACC AGC TAC TGG ATG CAT TGG GTG AGG CAG GCG CCT GGC CAA CGT CTA
T   S   Y   W   M   H   W   V   R   Q   A   P   G   Q   R   L>
      200      210      220      230      240
*      *      *      *      *
GAG TGG ATC GGA GAG ATT GAT CCT TCT GAG AGT AAT ACT AAC TAC AAT
E   W   I   G   E   I   D   P   S   E   S   N   T   N   Y   N>
      250      260      270      280      290
      *      *      *      *      *
CAA AAA TTC AAG GGA CGC GTC ACA TTG ACT GTA GAC ATT TCC GCT AGC
Q   K   F   K   G   R   V   T   L   T   V   D   I   S   A   S>
      300      310      320      330
*      *      *      *
ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC ACT GCG GTC
T   A   Y   M   E   L   S   S   L   R   S   E   D   T   A   V>
      340      350      360      370      380
      *      *      *      *      *
TAC TAT TGT GCA AGA GGG GGT TAC GAC GGA TGG GAC TAT GCT ATT GAC
Y   Y   C   A   R   G   G   Y   D   G   W   D   Y   A   I   D>
      390      400      410      420      430
*      *      *      *      *
TAC TGG GGT CAA GGC ACC CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG
Y   W   G   Q   G   T   L   V   T   V   S   S   A   S   T   K>
      440      450      460      470      480
      *      *      *      *      *
GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG
G   P   S   V   F   P   L   A   P   S   S   K   S   T   S   G>
      490      500      510      520
*      *      *      *
GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG
G   T   A   A   L   G   C   L   V   K   D   Y   F   P   E   P>
530      540
*      *
GTG ACG GTG TCG
V   T   V   S>

```

FIG. 3

```

      10      20      30      40
    *      *      *      *
ATG AAG TTG CCT GTT AGG CTG TTG GTG CTT CTG TTG TTC TGG ATT CCT
M  K  L  P  V  R  L  L  V  L  L  F  W  I  P>
      signal peptide cleavage site
50  BspE I  60  70  80  90
*      *      *      *      *      *
GTT TCC GGA GGT GAT GTT GTG ATG ACT CAA AGT CCA CTC TCC CTG CCT
V  S  G  G  D  V  V  M  T  Q  S  P  L  S  L  P>

100      110      120      130      140
*      *      *      *      *
GTC ACC CCT GGA GAA CCA GCT TCT ATC TCT TGC AGG TCT AGT CAG AGT
V  T  P  G  E  P  A  S  I  S  C  R  S  S  Q  S>

150      160      170      180 Asp 718 190
*      *      *      *      *
CTT GCA AAG AGT TAT GGG AAC ACC TAT TTG TCT TGG TAC CTG CAG AAG
L  A  K  S  Y  G  N  T  Y  L  S  W Y L  Q  K>

200      210      220      230      240
*Msc I*      *      *      *      *
CCT GGC CAG TCT CCA CAG CTC CTC ATC TAT GGG ATT TCC AAC AGA TTT
P  G  Q  S  P  Q  L  L  I  Y  G  I  S  N  R  F>

250      260      270      280
*      *      *      *
TCT GGG GTG CCA GAC AGG TTC AGT GGC AGT GGT TCA GGG ACA GAT TTC
S  G  V  P  D  R  F  S  G  S  G  S  G  T  D  F>

290      300 NruI      310      320      330
*      *      *      *      *
ACA CTC AAG ATC TCG CGA GTA GAG GCT GAG GAC GTG GGA GTG TAT TAC
T  L  K  I  S  R  V  E  A  E  D  V  G  V  Y  Y>

340      350      360      370      380
*      *      *      *      *
TGC TTA CAA GGT ACA CAT CAG CCG TAC ACG TTC GGA CAG GGG ACC AAG
C  L  Q  G  T  H  Q  R  Y  T  F  G  Q  G  T  K>

390      400      410 Kas I
*      *      *      *
GTG GAA ATA AAA CGG GCT GAT GCG GCG CC
V  E  I  K  R  A  D  A  A  P>

```

FIG. 4

Light Chain

CDR1 R S S Q S L A K S Y G N T Y L S

CDR2 G I S N R F S

CDR3 L Q G T H Q P Y T

Heavy Chain

CDR1 S Y W M H

CDR2 E I D P S E S N T N Y N Q K F K G

CDR3 G G Y D G W D Y A I D Y

FIG. 5

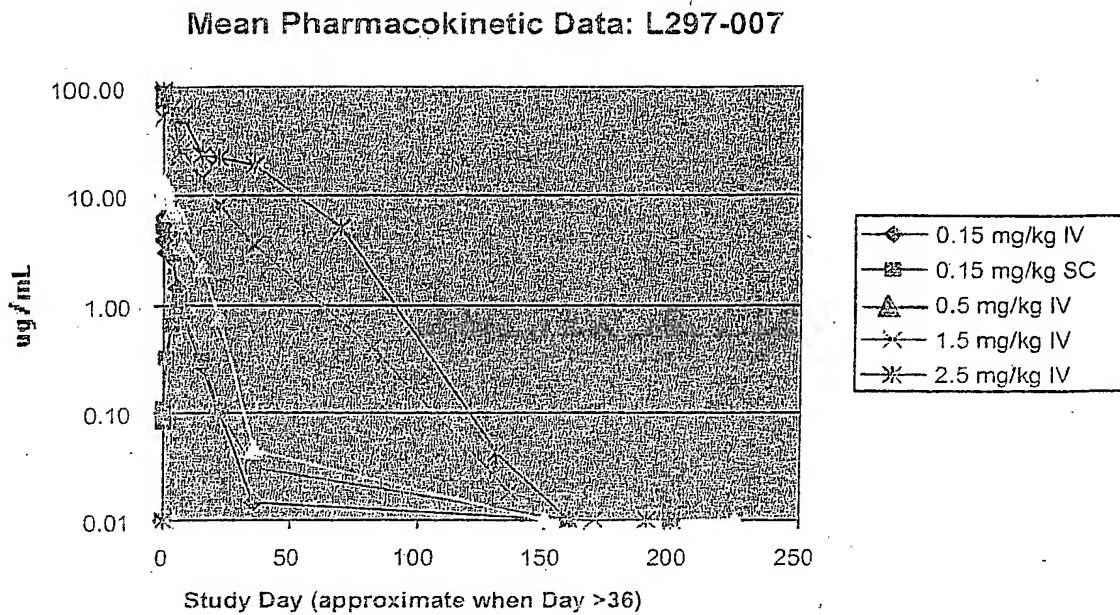


FIG. 6

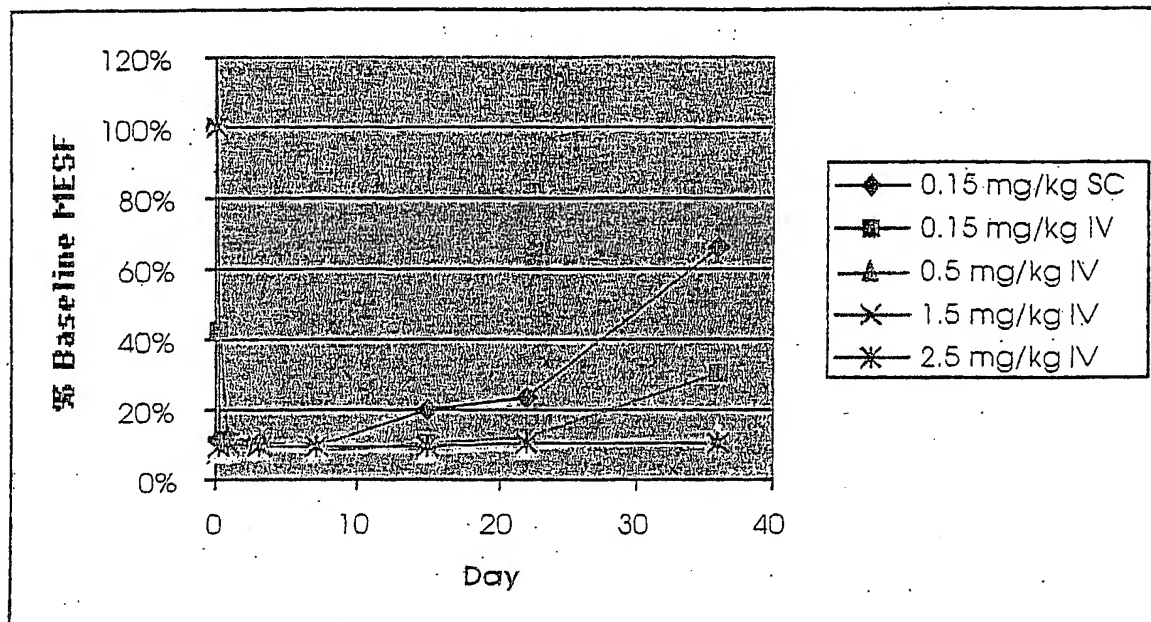


FIG. 7

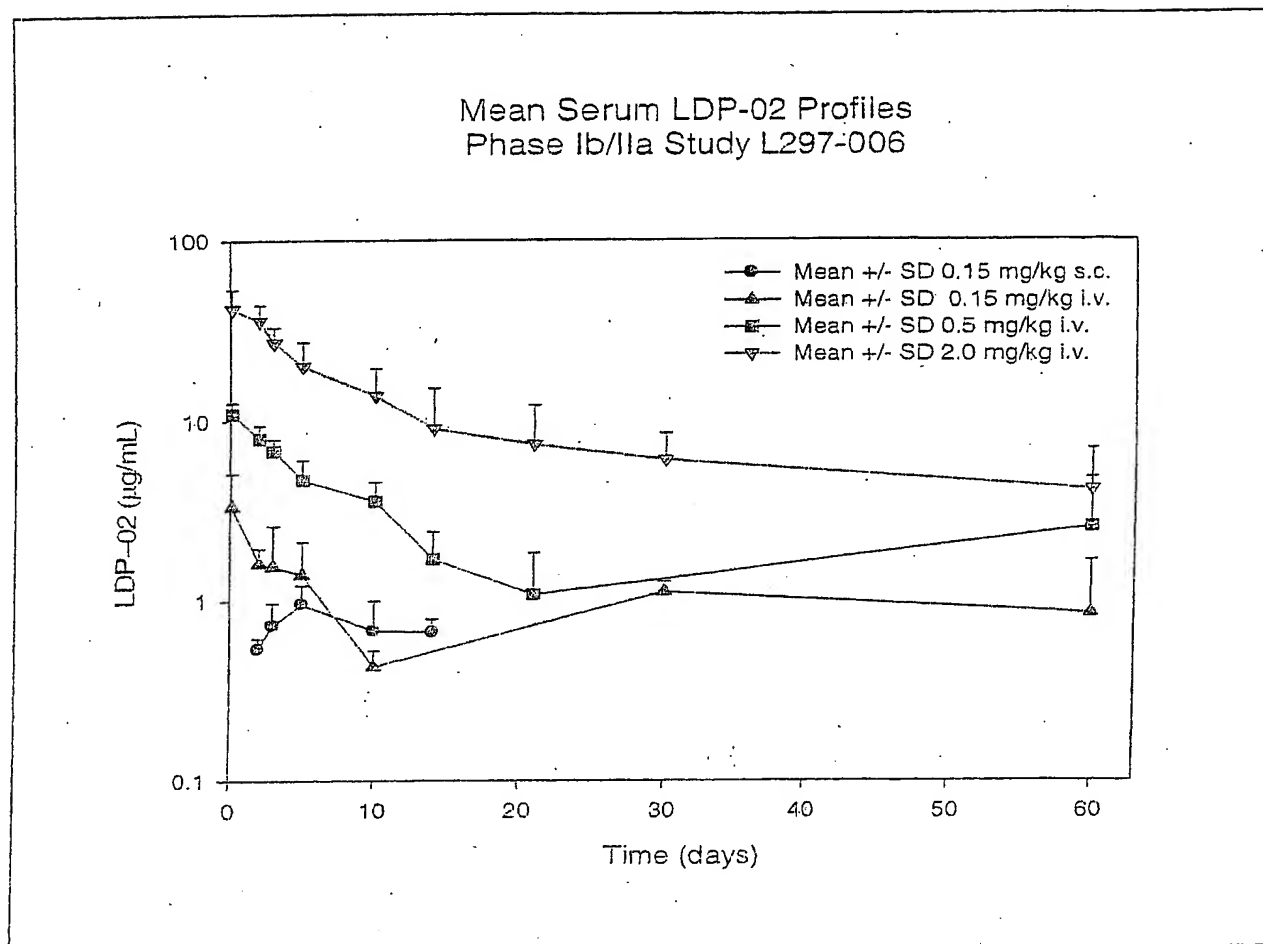


FIG. 8



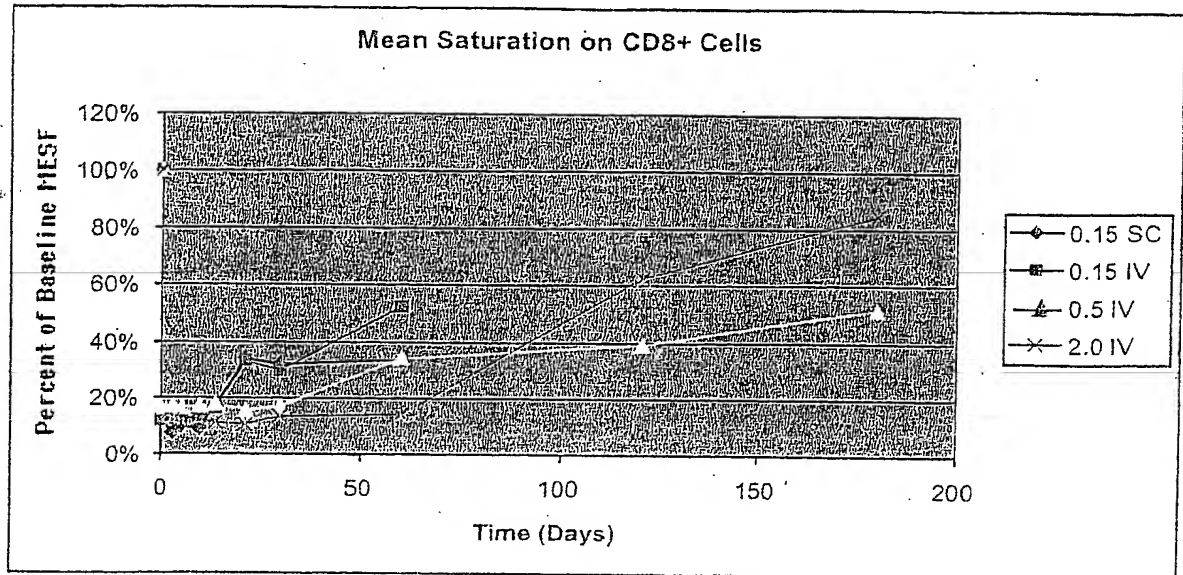


FIG. 9